



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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Limits		Index	History	Clipboard			
Display	Default View	<input type="text" value="as"/>	HTML	<input type="button" value="Save"/>	<input type="button" value="Add to Clipboard"/>		

1: P29449 THIOREDOXIN H-TYPE 1 (TRX-H1)

BLink, PubMed, Related Sequences, Taxonomy, LinkOut

LOCUS THH1_TOBAC 126 aa PLN 01-OCT-2000
 DEFINITION THIOREDOXIN H-TYPE 1 (TRX-H1).
 ACCESSION P29449
 PID g267124
 VERSION P29449 GI:267124
 DBSOURCE swissprot: locus THH1_TOBAC, accession P29449:
 class: standard.
 created: Apr 1, 1993.
 sequence updated: Apr 1, 1993.
 annotation updated: Oct 1, 2000.
 xrefs: gi: 20046, gi: 20047, gi: 100387
 xrefs (non-sequence databases): HSSP P10599, InterPro IPR000063,
 Pfam PF00085, PRINTS PR00421, PROSITE PS00194
 KEYWORDS Redox-active center; Electron transport; Multigene family.
 SOURCE common tobacco.
 ORGANISM Nicotiana tabacum
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
 I; Solanales; Solanaceae; Nicotiana.
 REFERENCE 1 (residues 1 to 126)
 AUTHORS Marty,I. and Meyer,Y.
 TITLE Nucleotide sequence of a cDNA encoding a tobacco thioredoxin
 JOURNAL Plant Mol. Biol. 17 (1), 143-147 (1991)
 MEDLINE 91329721
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. WHITE BURLEY

COMMENT

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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PARTICIPATES IN VARIOUS REDOX REACTIONS THROUGH THE
 REVERSIBLE OXIDATION OF THE ACTIVE CENTER DITHIOL, TO A DISULFIDE.
 THE H FORM IS KNOWN TO ACTIVATE A NUMBER OF CYTOSOLIC ENZYMES (BY
 SIMILARITY).
 [SUBCELLULAR LOCATION] CYTOPLASMIC (BY SIMILARITY).
 [SIMILARITY] BELONGS TO THE THIOREDOXIN FAMILY. PLANT H-TYPE.

FEATURES Location/Qualifiers
 source 1..126
 /organism="Nicotiana tabacum"
 /db_xref="taxon:4097"
 Protein 1..126
 /product="THIOREDOXIN H-TYPE 1"
 Bond bond(46,49)
 /bond_type="disulfide"
 /note="REDOX-ACTIVE (BY SIMILARITY)."

ORIGIN

1 maandatsse egqvfgchkv eewneyfkkv vetkklvvvd ftaswcgpcr fiapiladia
 61 kkmphviflk vdvdelktvs aewsveampt fvfkldgkev drvvgakkee lqgtivkhaa
 121 patvta

//



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search		Protein	for		Go			Clear
Limits		Index		History		Clipboard		
Display	Default View	as	HTML	Save	Add to Clipboard			

☐ 1: CAA94534 **thioredoxin [Ricinus communis]** [BLink, Related Sequences, Nucleotide, Taxonomy](#)

LOCUS CAA94534 118 aa PLN 04-APR-1996
 DEFINITION thioredoxin [Ricinus communis].
 ACCESSION CAA94534
 PID g1255954
 VERSION CAA94534.1 GI:1255954
 DBSOURCE embl locus RCTHIORXN, accession Z70677.1
 KEYWORDS .
 SOURCE castor bean.
 ORGANISM Ricinus communis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 Rosidae; Euphorbiales; Euphorbiaceae; Ricinus.
 REFERENCE 1 (residues 1 to 118)
 AUTHORS Szederkenyi, J., Dolgener, E. and Schobert, C.
 TITLE cDNA expressed in Ricinus cotyledons
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 118)
 AUTHORS Dolgener, E.
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-1996) Dolgener E., University of Bayreuth,
 Department of Plant Physiology, Universitaetsstr.30, Bayreuth,
 Germany, 95440
 FEATURES Location/Qualifiers
 source 1..118
 /organism="Ricinus communis"
 /cultivar="Sanguineus"
 /db_xref="taxon:3988"
 /clone="pEDRH018"
 /dev_stage="seedling"
 /tissue_type="cotyledon"
 /clone_lib="lambda Excell"
 Protein 1..118
 /product="thioredoxin"
 CDS 1..118
 /db_xref="SPTREMBL:Q43636"
 /coded_by="Z70677.1:23..379"
 ORIGIN
 1 maaeegqvig chtveawneq lqkgnndtkgl ivvdftaswc gpcrfiapfl aelakklpnv
 61 tflkvdvdel ktvahewave smptfmflke gkimdkvvga kkdelqqtia khmatast
 //

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Protein

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM	
Search		Protein	for		Go			Clear
Limits		Index		History		Clipboard		
Display	Default View	as	HTML	Save	Add to Clipboard			

1: P29448 THIOREDOXIN H-TYPE 1 (TRX-H-1)

BLink, PubMed, Related Sequences, Taxonomy, LinkOut

LOCUS THH1_ARATH 114 aa PLN 01-OCT-2000
DEFINITION THIOREDOXIN H-TYPE 1 (TRX-H-1).
ACCESSION P29448
PID g267122
VERSION P29448 GI:267122
DBSOURCE swissprot: locus THH1_ARATH, accession P29448:
class: standard.
created: Apr 1, 1993.
sequence updated: Apr 1, 1993.
annotation updated: Oct 1, 2000.
xrefs: gi: gi: 16551, gi: gi: 16552, gi: gi: 1388079, gi: gi: 1388080, gi: gi: 6782245, gi: gi: 6562255, gi: gi: 478400, gi: gi: 322606
xrefs (non-sequence databases): HSSP P80028, InterPro IPR000063, Pfam PF00085, PRINTS PR00421, PROSITE PS00194
KEYWORDS Redox-active center; Electron transport; Multigene family.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (residues 1 to 114)
AUTHORS Rivera-Madrid,R., Marinho,P., Brigidou,C., Chartier,Y. and Meyer,Y.
TITLE Nucleotide sequence of a cDNA clone encoding an Arabidopsis thaliana thioredoxin h
JOURNAL Plant Physiol. 102 (1), 327-328 (1993)
MEDLINE 94151431
REMARK SEQUENCE FROM N.A.
REFERENCE 2 (residues 1 to 114)
AUTHORS Sahrawy,M., Hecht,V., Lopez-Jaramillo,J., Chueca,A., Chartier,Y. and Meyer,Y.
TITLE Intron position as an evolutionary marker of thioredoxins and thioredoxin domains
JOURNAL J. Mol. Evol. 42 (4), 422-431 (1996)
MEDLINE 96215867
REMARK SEQUENCE FROM N.A.
STRAIN=CV. LANDSBERG ERECTA
REFERENCE 3 (residues 1 to 114)
AUTHORS Vitale,D., Liguori,R., Flores,M., Argiriou,A., De Simone,V., Mewes,H.-W., Lemcke,K., Mayer,K.F.X., Quetier,F. and Salanoubat,M.
TITLE Direct Submission
JOURNAL Submitted (??-NOV-1999) to the EMBL/GenBank/DDBJ databases
REMARK SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA
COMMENT
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[FUNCTION] PARTICIPATES IN VARIOUS REDOX REACTIONS THROUGH THE REVERSIBLE OXIDATION OF THE ACTIVE CENTER DITHIOL, TO A DISULFIDE. THE H FORM IS KNOWN TO ACTIVATE A NUMBER OF CYTOSOLIC ENZYMES (BY

SIMILARITY) .
[SUBCELLULAR LOCATION] CYTOPLASMIC (BY SIMILARITY) .
[SIMILARITY] BELONGS TO THE THIOREDOXIN FAMILY. PLANT H-TYPE.

FEATURES

source	Location/Qualifiers
	1..114
	/organism="Arabidopsis thaliana"
	/db_xref="taxon:3702"
Protein	1..114
	/product="THIOREDOXIN H-TYPE 1"
Bond	bond(40,43)
	/bond_type="disulfide"
	/note="REDOX-ACTIVE (BY SIMILARITY)."

ORIGIN

1	maseegqvia	chtvetwneq	lqkanesktl	vvvdftaswc	gpcrfiapff	adlakklpnv
61	lflkvdt del	kvsasdwaiq	amptfmflke	gkildkvvga	kkdelqstia	khla

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